

COMPOSITIONS AND METHODS FOR PARSING GENE STRUCTUREABSTRACT OF THE DISCLOSURE

- The invention provides a method for determining a sequence boundary. The method includes the steps of
- 5 (a) contacting a population of addressed fragments of eukaryotic genomic DNA with a target polynucleotide, the target polynucleotide binding a terminal sequence of a DNA region, the addressed fragments of eukaryotic genomic DNA being at least 100 nucleotides in length; (b)
  - 10 determining a relative order for 2 or more of the addressed fragments compared to a sequence of the genomic DNA; (c) identifying a pair of fragments among the 2 or more addressed fragments that alternatively bind the terminal sequence of a region; and (d) determining for
  - 15 the sequence of the genomic DNA a relative location of a boundary of the region compared to a location of at least one genomic DNA fragment in the pair.

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